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The present sequence is human metalloproteinase ADAWTS-9. The ADAWTS family of proteins is closely related to the ADAWS family and Metalloproteinase Domain; family, members of the ADAWTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAWS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzhaims's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migratedon, inflammation and/or anglosmesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour cachexia; inflammation, dermatosparaxis; EDS-VIIC; angiogenesi; Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human; metastasis; embryogenesis; egg implantation; ADAWIS-9.
                                                                                                                                                                                                                                                                                                                                            289 LSYPRFVEVLVVADDNRAVSYHGENLQHYILTLMSIVASIYKDPSIGNIINIVIVNLIVIH 348
                                                                                                                                                                                                                                                                                                                                                                                       61 NEODGPSISPNAOTTLKNPCOMOHSKNSPGGIHHDTAVLLTRODICRAHDKCDTLGLAEL 120
                                                                                                                                                                                                                                                                                                                                                                                                             149 NEGDGPSISFNAQTILKNLCQWQHSKNSPGGIHHDTAVLLTRQDICRAHDKCDTLGLAEL 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTICDPYRSCSISEDSGLSTAPTIAHELGHVPNMPHDDNNKCKEEGVKSPQHVMAPTLNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 GTICDPYRSCSISBDSGLSTAFTIAHELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNF 468
                                                                                                                                                                                                                                                                                                                        1 LSYPREVEVLVVADNRAVSYHGENLQHYILTLASIVASIYKDPSIGNLINIVIVNLIVIH 60
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                                                                                                                                                                                                                                                        Length 1073;
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                                                                                                                                                                                                                                                     Query Match
99.4%; Score 1025; DB 21;
Best Local Similarity 99.5%; Pred. No. 2.9e-106;
Matches 189; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ADAMTS-9 amino acid sequence.
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(APT'S), APT'S S S.
(HURS/) HURSKAINEN T L.
(HIRO/) HIROHATA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000WO-US21223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 YINPWMWSKC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 YTNPWMWSKC 478
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AAB72286
ID AAB7
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AC AAB7
DT 14-b
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DE HUMI
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KW ADA
KW ADA
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'A Disintegrin-like And Metalloprotease domain with

WPI; 2001-159978/16.

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This invention relates to murine and human ADAMTS-N (A disintegrin-like and metalloprotease domain with thrombospondin type I motifs) proteins, designated ADAMTS-S, 6, 7, 8, 9, 10 and Rt. Also included in the invention are CDNA sequences encoding the proteins, and antibodies specific for the proteins. The mucleic acid sequences and proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate ADAMTS-N expression. Disorders that may be treated using the nucleic acids, proteins and antibodies incattle or Ehlers-banlos syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage in arthritic (both inflammatory and non-inflammatory) disease, angiogenesis, tumour growth and metastases, and they may also be used for controlling embryogenests and implantation of fertilised eggs. The present sequence represents human ADAMTS-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSYPREVEVLVVADDRAWSYHGENLQHYILIILMSIVASIYKDPSIGNLINIVIVNLIVIH 60
them, useful for treating e.g. tumours, inflammation and arthritis
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98.5%; Score 1015.5; DB 22; Length 1882;
Best Local Similarity 99.5%; Pred. No. 7.6e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ADAMTS-9 alternative amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72301 standard, Protein; 1934 AA.
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                                               Claim 1, Fig 7; 181pp; English
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(APTE/) APTE S S.
(HURS/) HURSKAINEN T
(HIRO/) HIROHATA S.
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This invention relates to murine and human ADAWIS-N (A disintegrin-like and metallogrotease domain with thrombospondin type I motifs) proteins, designated ADAWIS-5, 6, 7, 8, 9, 10 and R1. Also included in the invention are CDNA sequences enading the proteins, and antibodies specific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate ADAWIS-N expression. Disorders that may be treated with inappropriate ADAWIS-N expression. Disorders that may be treated using the nucleic acids, proteins and antibodies include, for example using the nucleic acids, proteins and antibodies include, for example using the vire (EDS-VIIC) in humans, erosion of articular cartilage in atthitic (both inflammatory and non-inflammatory) disease, and their may also be used for controlling embryogenesis and implantation of fertilised eggs. The
                                                                              Murine and human 'A Disintegrin-like And Metalloprotesse domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -
                                                                                                                                                                                                   Disclosure, Fig 17; 181pp, English
2001-159978/16.
                           N-PSDB, AAF63449.
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1934 AA; Sequence

Gaps 98.5%; Score 1015.5; DB 22; Length 1934; 99.5%; Pred. No. 7.9e-105; ive 0; Mismatches 0; Indels 1; Q Best Local Similarity 99.5 Matches 189, Conservative Query Match

289 LSYPRFVEVLVVADNRMVSYHGENLQHYILTIMSIVASIYKDPSIGNLINIVIVNLIVIH 348 120 1 LSYPREVEVLVVADNRMVSYHGENLQHYILTIMSIVASIYKDPSIGNLINIVIVNLIVIH 61 NEQDGPSISFNAQTTLKNPCQWQHSKNSPGGIHHDTAVLLTRQDICRAHDKCDTLGLAEL ઠે d ઠે

GTICDPYRSCSISEDSGLSTAFTIAHELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNF 180 407 121 음

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AAB72287

AAB72287 standard, Protein, 874 AA.

AAB72287;

(first entry) 14-MAY-2001

Murine ADAMIS-9 amino acid sequence.

ADAWIS-N; disintegrin; metalloprotease; thrombospondin type I motif; tumour cachexia; inflammation; dermatosparaxis; EDS-VIIC; angiogenesis Enlers-Danlos syndrome type VIIC; articular cartilage erosion; mouse; metastasis; embryogenesis; egg implantation; ADAWTS-9

Mus musculus.

#0200111074-A2.

15-FEB-2001

2000WO-US21223 03-AUG-2000; 

99US-0369364 06-AUG-1999;

CLEVELAND CLINIC FOUND APTE S CLEV-) (APTE/)

(APTE/) APTE S S. (HURS/) HURSKAINEN (HIRO/) HIROHATA S.

Hirohata S; Hurskainen TL, Apte SS,

WPI; 2001-159978/16 N-PSDB; AAF63444 Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -

Claim 1; Fig 8; 181pp; English

This invention relates to murine and human ADAWTS-N (A disintegrin-like and metalloprotease domain with thrombospondin type I motifs) proteins, designated ADAWTS-5, 6, 7, 8, 9, 10 and R1. Also included in the invention are CDNA sequences encoding the proteins, and antibodies specific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate ADAMTS-N expression. Disorders that may be treated using the nucleic acids, proteins and antibodies include, for example tumour cachexia, inflammation, dermacosparaxis in cattle or Ehlers-Danlos syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage in arthritic (both inflammatory and non-inflammatory) disease, controlling embryogenesis and implantation of fertilised eggs. The present sequence represents murine ADAMTS-9.

874 AA; Seguence

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Gaps ö Score 947; DB 22; Length 874; Pred. No. 1.4e-97; 8; Mismatches 8; Indels ( 91.98; 91.68; Best Local Similarity 91.6 Matches 174, Conservative Query Match

1 LSYPRFVEVLVVADNRMVSYHGENLQHYILTLMSIVASIYKDPSIGNLINIVIVNLIVIH 60 ठे 셤

247 61 NEQDGPSISFNAQTTIKANFCQWQHSKNSPGGIHHDTAVLLIRQDICRAHDKCDTLGLAEL 120 ò 쉼

GTICDPYRSCSISEDSGLSTAFTIAHELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNF 180 248 GTICDPYRSCSISEDSGLSTAFTIAHELGHVFNMPHDDSNKCKEEGVKSPOHVMAPTINF 121 ò 요

YINPWMWSKC 190 181

ਨੇ 셤

308 YTNPWMWSKC 317

RESULT 11

AAU77133 standard; Protein; 1907 AA. AAU77133;

Human protease #12.

05-JUN-2002

Human; protease; enzyme

Homo sapiens 

WO200216564-A2 28-FEB-2002.

22-AUG-2001; 2001WO-US26148

19-287

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DAG

The invention relates to an isolated human protease polypeptide (PRTS).

PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastritis, cirrhosis, Crohn's disease), autoimmune/inflammatory disorders (AIDS, allergy, rheumatorid arthritis, annemia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hypertension, epithelial disorder (vitiligo, keloid, eczema), neurological disorders (circhis), adisorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease, proteone of a tissue or cell type, PRTS protein is useful in a number of drug screening techniques and to callapse the proteome of a tissue or cell type. PRTS NRA is useful for creating knockin humanised animals or transgenic animals to model human ulising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PRTS-10 protein. Human PRTS-10

1916 AA; Sequence

Gaps MGSPDAAAAVRKDRLHPRQVKLLETLSEYBIVSPIRVNALGEPFPTNVHFKRTRRSINSA 61 .. 0 Length 1916; Indels Query Match 99.6%; Score 1405; DB 23; Best Local Similarity 100.0%; Pred. No. 4.2e-139; Matches 268; Conservative 0; Mismatches 0; N ઠ 유

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121 9 TDPWPAFASSSSSSTSSQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLGTPGVNQTKF 62 ઠે

120 181 61 TDPWPAFASSSSSSTSSQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLGTPGVNQTKF YSEEBAELKHCFYKGYVNTNSEHTAVISLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEEB 122 121 셤 ઠે 셤

180 241 240

QNKPHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALNS 181 QNKPHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALNS 182 ò 쉱

AAB72301 RESULT

AAB72301 standard; Protein; 1934 AA D X B X S X X X X X X X B X B X Y X Y X

(first entry) 14-MAY-2001 AAB72301;

Human ADAMTS-9 alternative amino acid sequence.

ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif; tumour cachexia; inflammation; dermatosparaxis; EDS-VIIC; anglogenesis; Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human; metastasis; embryogenesis; egg implantation; ADAMTS-9.

Homo sapiens

WO200111074-A2

15-FEB-2001.

03-AUG-2000; 2000WO-US21223.

99US-0369364. MG-1999;

LAND CLINIC FOUND.

(HURS/) HURSKAINEN T L. (HIRO/) HIROHATA S. 

Hirohata S; Hurskainen TL, Apte SS,

2001-159978/16. N-PSDB; AAF63449 Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -

Disclosure; Fig 17; 181pp; English.

and metalloprotested domain with thrombospondin type I motife) proteins, designated ADAMTS-5, 6, 7, 8, 9, 10 and R1. Also included in the invention are cDNA sequences-encoding the proteins, and antibodies specific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, diagnosis and treatment of diseases associated using the nucleic acids, proteins. Disorders that may be treated using the nucleic acids, proteins and antibodies include, for example tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage angiogenesis, tumour growth and metastases, and they may also be used for present sequence represents human ADAMTS-9. invention relates to murine and human ADAMTS-N (A disintegrin-like

1934 AA; Seguence

Gaps ó, Length 1934; Indels 99.1%; Score 1398; DB 22; 99.3%; Pred. No. 2.4e-138; iive 0; Mismatches 2; Query Match
Best Local Similarity 99.3'
Matches 267; Conservative

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78 1 EMGSPDAAAAVRKDRLHPRQVKLLETLSEYEIVSPIRVNALGEPFPTNVHFKRTRRSINS 60 19 EMGSPDAAAAVRKDRLHPRQVKLLETLSEYEIVSPIRVNALGEPPPTNVHFKRTRRSINS ð 셤

ATDPWPAFASSSSSSTSSQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLGTPGVNQTK 120 ATDPWPAFASSSSSSSSPQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLGTPGVNQTK 138 4 61 셤 ò

FYSEBEALLKHCFYKGYVNTNSEHTAVISLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEE 180 121 139 à 셤

240 EQNKPHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKMGERINLAGDVAALN EQNKPHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALN 181 ठ 셤

258

259 SGLATEAFSAYGNKTDNTREKRTHRIKR 287 241 SGLATEAFSAYGNKTDNTREKRTHRRTKR 269 ò 셤

199

σ ABG30702

ABG30702 standard; Protein; 1602 AA. ABG30702; 

(first entry) 07-OCT-2002

Human aggrecanase polypeptide #1.

computer aided drug design, osteoarthritis, proteolytic activity, articular cartilage; Human, aggrecanase, enzyme, aggrecan, genetic disorder, osteopathic, antiarthritic.

Homo sapiens

Key

Location/Qualifiers

erosion; human;

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                                                                                                                                                                                                                                                                                                                                                                                                           Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -
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Ehlers-Danlos syndrome type VIIC; articular cartilage metastasis; embryogenesis; egg implantation; ADAMTS-9.
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Pred. No. 0;
2; Mismatches
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Rest Local Similarity 99.3%;
Atches 1612; Conservative
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HURSKAINEN T L.
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                                                                                                                       SEDSGLSTAFTIAHELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNFYTNPMMSKCSR
                                                                                                                                                                                                 KYITEFLDTGYGECLLNEPESRPYPLPVQLPGILYNVNKQCELIFGPGSQVCPYMMQCRR
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                           SEDSGLSTAFT1AHELGHVFNMPHDDNNKCKEEGVKSPOHVMAPTLNFYTNPWMWSKCSR
QTTLKNFCQWQHSKNSPGG1HHDTAVLLTRQD1CRAHDKCDTLGLAELGT1CDPYRSCSI
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AWSTGPWSSCSVSCGRGHKQRNVYCMAKDGSHLESDYCKHLAKPHGHRKCRGGRCPK
                          1440 HDAAWSTGPWSSCSVSCGRGHKQRNVYCWAKDGSHLESDYCKHLAKPHGHRKCRGGRCPK
                                                                         WKAGAWSQCSVSCGRGVQQRHVGCQIGTHKIARETECNPYTRPESERDCQGPRCPLYTWR
                                                                                                   1500 WKAGAWSQCSVSCGRGVQQRHVGCQIGTHKIARDTECNPYTRPESECECQGPRCPLYTWR
                                                                                                                                                      AEEWQECTKTCGEGSRYRKVVCVDDNKNEVHGARCDVSKRPVDRESCSLQPCEYVWITGE
                                                                                                                                                                             1560 AEESQECTKTCGEGSRYRKVVCVDDNKNEVHGARCDVSKRPVDRESCSLQPCEYVWITGE
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RESULT 5

AAE19173 standard, Protein; 1916 AA

AAE19173;

(first entry) 21-MAY-2002

Human protease, PRTS-10 protein.

gastrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AIDS; Acquired Immune Deficiency Syndrome; allergy; rheumatoid arthritis; anaemia; asthma; atherosclerosis; hypertension; myocardial infarction; hepatitis; cancer; psoriasis; Cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; Pick's disease; infertility; vitiligo; drug screening; gene therapy; gastritis; cirrhosis; Crohn's disease; Human; protease; PRTS-10; enzyme;

Homo sapiens.

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/note= "Thrombospondin type I domain"
1313..1364
/note= "Thrombospondin type I domain"
/1426..1479
/note= "Thrombospondin type I domain" Location/Qualifiers Key Domain Domain Domain

WO200208396-A2

31-JAN-2002

17-JUL-2001; 2001WO-US22397 21-JUL-2000; 

2000US-221680P. 2000US-223544P. 2000US-224717P. 2000US-225988P. 2000US-227568P 28-JUL-2000; 04-AUG-2000; 11-AUG-2000; 16-AUG-2000; 23-AUG-2000;

(INCY-) INCYTE GENOMICS INC

Todd ne AM, Gandhi AR, Hafalia AJA, Lu DAM, Patterson C; 3Y CM, Das D, Kallick DA, Nguyen DB, Lee EA, Khan FA; Au-Young J, Griffin JA, Pollcky JL, Ramkumar J, Yang J; Blu K, Ding L, Kaarney L, Baughn MR, Borowsky ML; ala MS, Yao MG, Burford N, Walia NK, Lal P, Lee S, Todd Tang YT, Elliott VS, Azimzai Y, Lu Y; Thangavelu K, Ding L, Kearney L, Baughn Sanjanwala MS, Yao MG, Burford N, Walia Lo TP, Tang YT, Elliott VS, Azimzai Y, Delegeane AM, Tribouley CM, Yue H,

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PKNGGKYCVGRRMKFKSCNTEPCLKQKRDFRDEQCAHFDGKHFNINGLLPNVRWVPKYSG

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2002-206082/26. N-PSDB; AAD30577 New human protease polypeptide, useful in diagnosis, prevention and

treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial and neurological disorders

Page 143-147; 182pp; English

The invention relates to an isolated human protease polypeptide (PRTS).

PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastritis, cirrhosis, Crohn's disease), autoimmune/inflammatory disorders (AIDS, allergy, rheumatoid arthritis, anaemia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer, psoriasis), developmental disorders (Ucubing's syndrome, hypothyroidism), epithelial disorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Porotein is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, in momental gene therapy and in microarrays utilising fluids or tissues from parients to detect altered PKIN expression. The present sequence is human PRTS-10 protein. Human PRTS-10 cycles. 

1916 AA; Sequence ö

139 199 259 240 319 300 360 439 420 499 480 619 559 540 Gaps 79 9 20 MGSPDAAAAVRKDRLHPRQVKLLETLSEYEIVSPIRVNALGEPFPTNVHFKRTRRSINSA TDPWPAFASSSSSSTSSQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLGTPGVNQTKF TDPWPAFASSSSSSSSSQAHYRLSAFGQQFLFNLTANAGFLAPLFTVTLLGTPGVNQTKF YSEERAELKHCFYKGYVNTNSEHTAVISLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEEE GLATEAFSAYGNKTDNTREKRTHRRTKRFLSYPRFVEVLVVADNRWVSYHGENLQHYILT FINAPHDDNNKCKEEGVKSPQHVMAPTLNFYTNPWMWSKCSRKYITEFLDTGYGECLLNEP WADGTECEPGKHCKYGFCVPKEMDVPVTDGSWGSWSPFGTCSRTCGGGIKTAIRECNRPE ONKPHIIYRRSAPOREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALNS LMSIVASIYKDPSIGNLINIVIVNLIVIHNEQDGPSISFNAQTTLKNFCQWQHSKNSPGG GLATEAFSAYGNKTDNTREKRTHRRTKRFLSYPRFVEVLVVADNRMVSYHGENLQHYILT IHHDTAVLLTRQDICRAHDKCDTLGLAELGTICDPYRSCSISEDSGLSTAFTIAHELGHV FINMPHDDNNKCKEEGVKSPQHVMAPTLNFYTNPWMWSKCSRKYITEFLDTGYGECLLNBP BSRPYPLPVOLPGILYNVNKQCELIFGPGSQVCPYMMQCRRLWCNNVNGVHKGCRTQHTP ESRPYPLPVQLPGILYNVNKQCELIFGPGSQVCPYMMQCRRLWCNNVNGVHKGCRTQHTP ; 0 Length 1916; Indels 23; 0 DB Score 8985; DB Pred. No. 0; 1; Mismatches 98.6%; Best Local Similarity 99.9 Matches 1603; Conservative Query Match 140 80 61 200 181 260 241 320 301 380 361 440 200 481 260 421 à g à g à 셤 g ò 요 ò 셤 à g ò 셤 ò ò 셤 ò 유